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FVQR  
PCRRDSPTTCGCPCCRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRA  
CRCRTGFF  
AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSA  
SSSSSEQCQPHRNCTALGLA  
LNVPGSSSHDTLCTSCTGFPILSTRVPGAE  
ECERAVIDFVA  
FQDISIKRLQRLLQALEAPE  
GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLV  
RLLQALRV  
ARMPGLERSVRERFLPVH

Fig. 1

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GGCTGGGTCCGACACCAAGGGGGCGCCGCGCCCTTGCAAGCTGCCTGGGCTG  
CTCACGGAGCTCCTGGGGCGCAGGACGGGGCGCTGCTGGTGCCTGCAAGGCGCTG  
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Fig. 2

CCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG  
CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCCCTGTGNGG  
GGAGCGTGACGGAGGAGGCACGGCTTGCCACGCCACCAACCGTGCCT  
GCCGCTGCCGCACCGGCTTCTCGCGCACGCTGGTTCTGCTGGAGCAC  
GCATCGTGTCCACCTGGTGCCTGGCGTGATTGCCCCGGGCACCCCCAGCCA  
GAACACGCAGTGCCTAGCGTGCACCCCCAGGCACCTCTCAGCCAGCAGC  
TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT  
GGCCCTCAATGTGCCAGGCTCTCCCTCCATGACACCCCTGTGACCAGCT  
GCACTGGCTTCCCCCTCAGCACCAAGGTACCAAGGAGCTGAGGAGTGAG  
CGTGCCGTATCGACTTGTGGCTTCCAGGACATCTCCAT

Fig. 3

Fig. 4.

SEQ ID No:4	178	CA-TTCTGGAACCTGGAGGCC
SEQ ID No:5	51	CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGN
SEQ ID No:6	2	CAGTTCTGGAACCTGGAGGCCGCTACTGCAACGTCCTCTG
SEQ ID No:3	51	CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGN
SEQ ID No:5	101	GGAGCNTGAGGAGGGCANGNGCTTGCACGCCACAAACGGCGCT
SEQ ID No:6	52	GGAGCGTGAAGGAGGGCACGGGCAAGGGCTTGCACGCCACAAACCGTGCCT
SEQ ID No:7	1	GAGGGGCCAGGAGTGGTGGGGGAGGGT
SEQ ID No:3	101	GGAGCGTGAAGGAGGGCACGGCTTGCACGCCACAAACCGTGCCT
SEQ ID No:5	151	GCGNGCTGCAGCCGGNTTCTTCGGCACGGCTGNTTTCTGCTTGGAGCAC
SEQ ID No:6	102	GCGGCTGCCGCCACGGGCTTCTTCGGCACGGCTGGTTCTGCTTGGAGCAC
SEQ ID No:7	32	TGGCAGGGGTCAGGTTGCTGGTCCAGGCTTGCACCTGAGCTAGGACAC
SEQ ID No:3	151	GCGGCTGCCACGGCTTCTTCGGCACGGCTTCTGCTTGGAGCAC
SEQ ID No:5	201	GCATCGTGTCCACCTGGTGNCGGGTGATTGNCNGGGCACCCCCAGCCA
SEQ ID No:6	152	GCATCGTGTCCACCTGGTGGCCGGGTGATTNCNGGGCACCCCCAGCCA
SEQ ID No:7	82	CAGTCCCTGACCCCTGTTCTCCCTCCTGGCTGCAGGCCACCCCCAGCCA
SEQ ID No:8	1	GCATCGTGTCCACCTGGTGGCCGGGTGATTGCCCCGGCACCCCCAGCCA
SEQ ID No:10	1	CTTGTCTCACCTGGTGGCCGGTGAATTNCACCCCCAGCCA
SEQ ID No:3	201	GCATCGTGTCCACCTGGTGGCCGGTGAATTGCCCCGGCACCCCCAGCCA

SEQ ID No: 5	251	GAACACGCA-TGCAAAGCCGTG
SEQ ID No: 7	132	GAACACGGCAGN-CC-AGCCGTGCCCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID No: 8	51	GAACACGGCAG-CCCTAGCCGTGCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID No: 10	47	GAACACGGCAGTGCC-AGCCNT-CCCCCAGGCCACCTTCTCAGCCAGCAGC
SEQ ID No: 9	1	AGCNGTGCNCNCAGGCACCTTCTCAGCCAGCAGT
SEQ ID No: 3	251	GAACACGGCAGTGCCTAGGCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID No: 7	182	TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCT
SEQ ID No: 8	101	TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCT
SEQ ID No: 10	97	TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGNC-T
SEQ ID No: 9	36	TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCT
SEQ ID No: 3	301	TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCT
SEQ ID No: 7	232	GGCCCTCAATGTGCCAGGGCTCTCCCATGACACCCCTGTGCACCCAG
SEQ ID No: 8	151	GGCCCTCAATGTGCCAGGGCTCTCCCATGACACCCCTGTGCACCCAGCT
SEQ ID No: 10	147	GGCCCTCAATGTGCCAGGGCTCTCCCATGACACCCCTGTGCACCCAGCT
SEQ ID No: 9	86	GGCCCTCAATGTGCCAGGGCTCTCCCATGACACCCCTGTGCACCCAGCT
SEQ ID No: 3	351	GGCCCTCAATGTGCCAGGGCTCTCCCATGACACCCCTGTGCACCCAGCT
SEQ ID No: 10	197	GCACGGCTCCCCCTCAGCACCCAGGTACCGGAGCTGAGGAGTGTGAG
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SEQ ID No: 3	401	GCACGGCTCCCCCTCAGCACCCAGGTACCGGAGCTGAGGAGTGTGAG
SEQ ID No: 10	247	CGTGGCTCATCGACCTTGTGGCTTCCAGGACATCTCCAT
SEQ ID No: 9	186	CGTGGCGTCACTCGACCTTGTGGCTTCCAGGACATCTCCAT
SEQ ID No: 3	451	CGTGGCGTCACTCGACCTTGTGGCTTCCAGGACATCTCCAT

Fig. 4. (Cont.)

DNA 30942  
hINFR2

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1 MAP V A V W A A L A V G L E L W A A A H A L P A O V A F T P Y A P E P G S T C A L R E Y Y D Q I

DNA 30942  
hINFR2

15 E R L V C A O C P P C T F V O R P C R R O S P T T C G P C P P R H Y T O F W H Y L E R C R Y C N V L  
50 A Q M C C S K C S P G O H A K V F C T K T S D T V C D S C E O S T Y T O L W N W V P E C L S C G S R

DNA 30942  
hINFR2

95 C G E R E E E A R A C H A T H N R A C R C R T G F F - - - A H A G - - F C L E H A S C P P G A G V  
100 C S S D O Q V E T O A C T R E O N R I C T C R P G W Y C A L S K O E G C R L C A P L R K C R P G F G V

DNA 30942  
hINFR2

139 1 A P G T P S Q N T Q C Q P C P P G T F S A S S S S S E O C O P H R N C T A L G L A L N V P G S S S  
150 A R P G T E T S D V V C K P C A P G T F S N T T S S T D I C R P H O I C H V V A - - - I P G N A S

DNA 30942  
hINFR2

189 H O T L C T S C T G F P L S T R V P G A E E C E R A V I D F V A F Q D I S I K R L O R L Q A L E A  
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DNA 30942  
hINFR2

229 P E G W G P T P - - R A G R A A L O L K L R R R L T E L G A Q D G A L L V R L L Q A L R V A R M P  
244 P M G P S P P A E G S T G D F A L P V G L I V G V T A L G L L I I G V V N C V I M T O V K K K P L - - -

DNA 30942  
hINFR2

287 G L E R S V R E R F L P V H  
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hINFR2

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hINFR2

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hINFR2

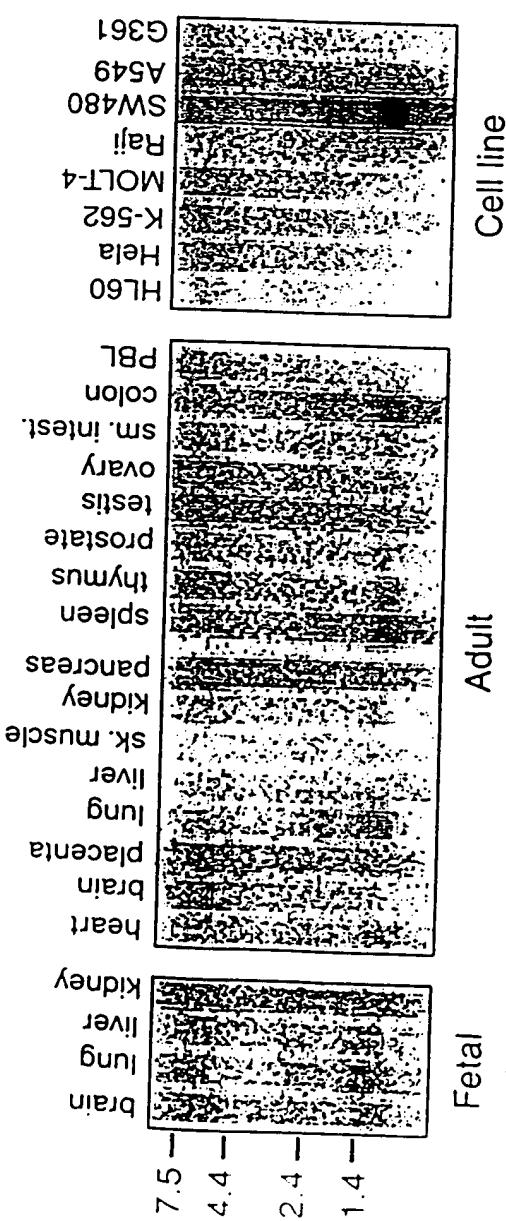
443 S T E E K P L P L G V P D A G M K P S

Fig. 5

DcR3	1	M R A L E G P G L S L L C L V L A L P A L L P V P A V R G V A	31
OPG	1	M N K L L C C A L V F L D I S I K W T T Q E T F P - - - - -	25
CRD1			
DcR3	32	E T P T Y P W R D A E T G E R L V C A Q C P P G T F V Q R P C	62
OPG	26	- - P K Y L H Y D E E T S H Q L L C D K C P P G T Y L ' K Q H C	54
CRD2			
DcR3	63	R R D S P T T C G P C P P R H Y T Q F W N Y L E R C R Y C N V	93
OPG	55	T A K W K T V C A P C P D H Y Y T D S W H T S D E C L Y C S P	85
CRD3			
DcR3	94	L C G E R E E E A R A R A C H A T H N R A C R C R T G F F A H A G	124
OPG	86	V C K E L Q Y V K Q E C N R T H N R V C E C K E G R Y L E I E	116
CRD4			
DcR3	125	F C L E H A S C P P G A G V I A P G T P S Q N T Q C Q P C P P	155
OPG	117	F C L K H R S C P P G F G V V Q A G T P E R N T V C K R C P D	147
CRD5			
DcR3	156	G T F S A S S S S S E Q C Q P H R N C T A L G L A L N V P G S	186
OPG	148	G F F S N E T S S K A P C R K H T N C S V F G L L L T Q K G N	178
CRD6			
DcR3	187	S S H D T L C T S C T G F P L S T R V P G A E E C E R A V I D	217
OPG	179	A T H D N I C S G N S E S T Q K C G I D - V T L C E E A F F R	208
CRD7			
DcR3	218	F V A F Q D I S I K R L Q R L L Q A L E A P E G W G P T - P R	247
OPG	209	F A V P T K F T P N W L S V L V D N L P G T K V N A E S V E R	239
CRD8			
DcR3	248	A G R A A L Q L K L R R R L T E L L G A Q D G A L - L V R L L	277
OPG	240	I K R Q H S S Q E Q T F Q L L K L W K H Q N K A Q D I V K K I	270
CRD9			
DcR3	278	Q A L R V A R M P G L E R S V R E R F L P V H 300	
OPG	271	I Q D I D L C E N S V Q R H I G H A N L T F E 293...	

Fig. 6

Fig. 7



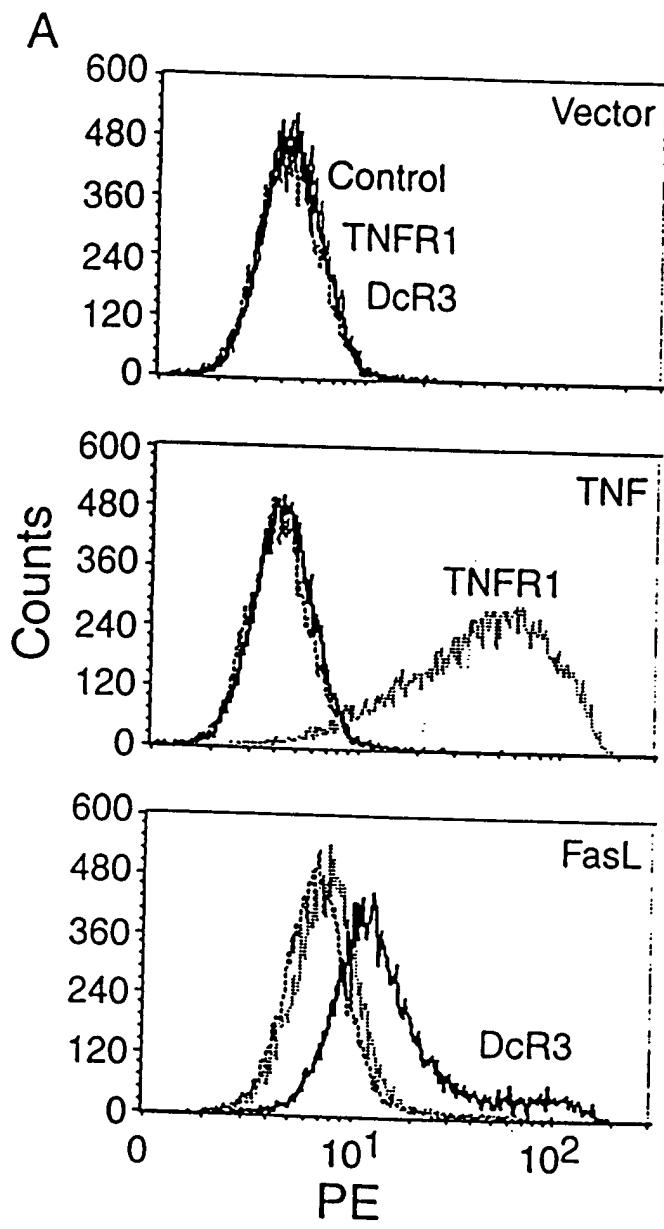
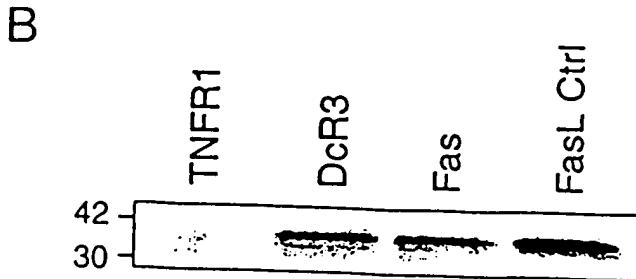


Fig. 8



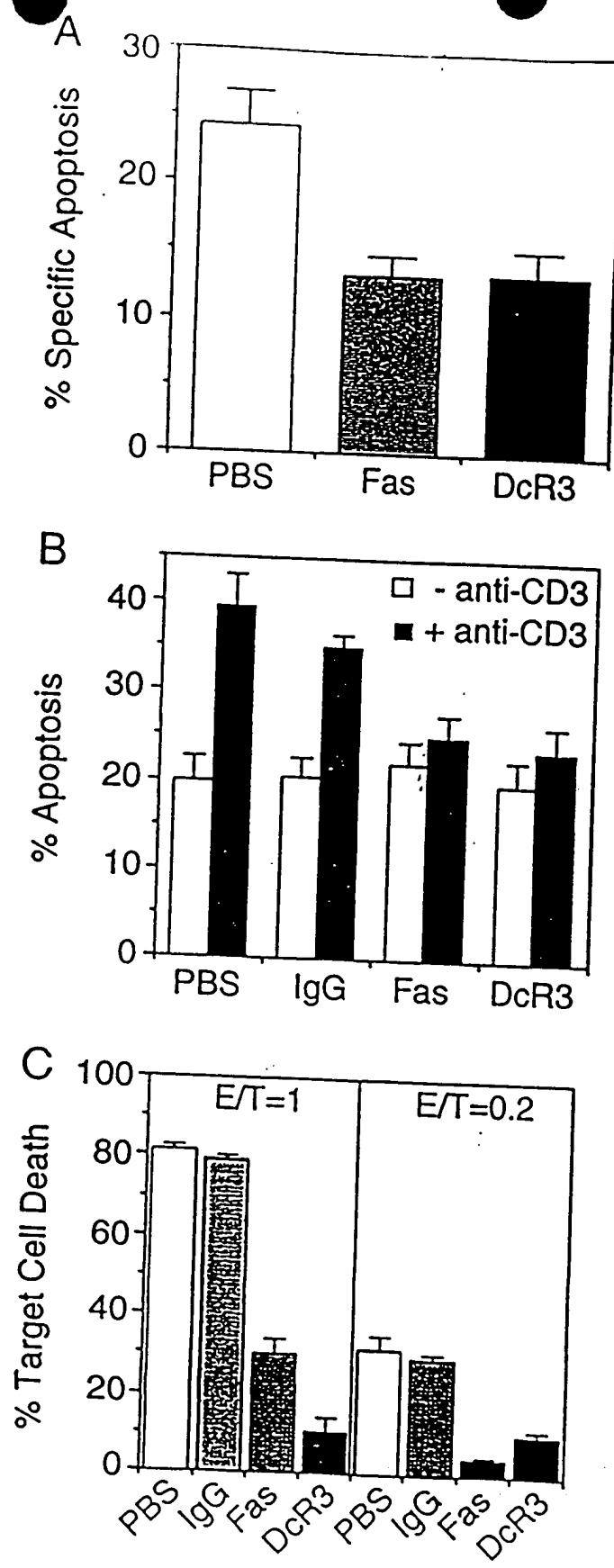


Fig. 9

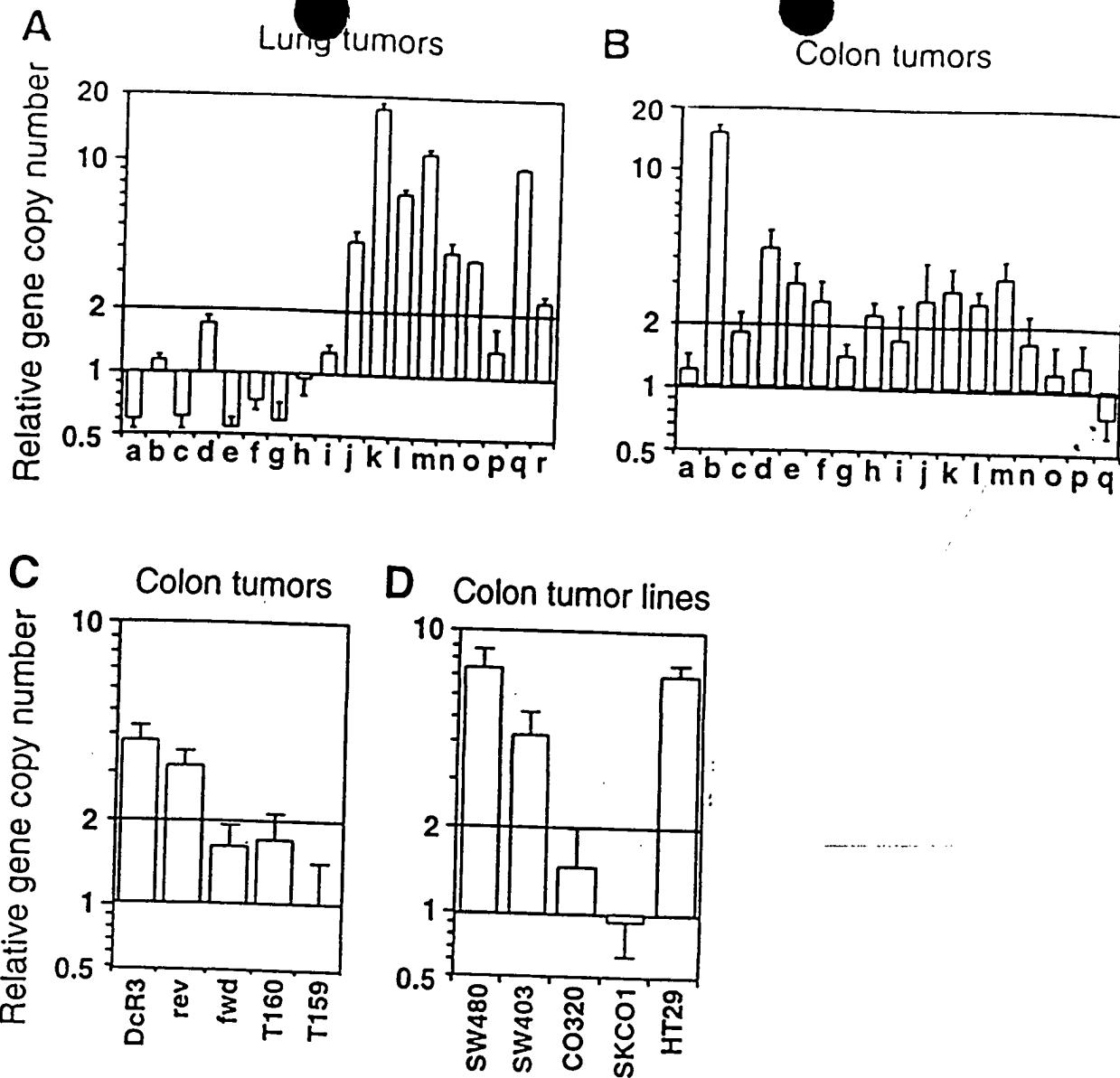


Fig. 10

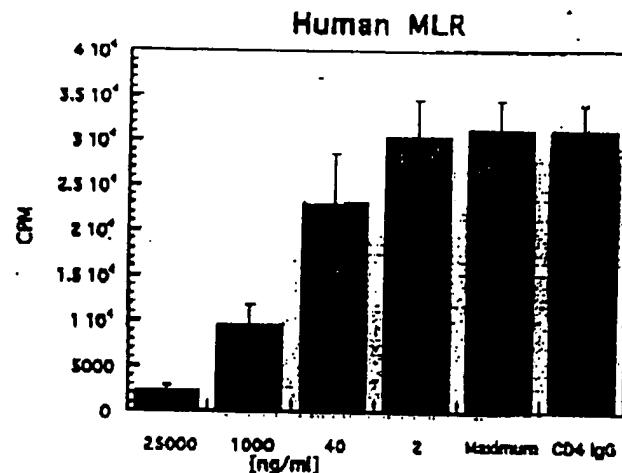


Fig. 11A

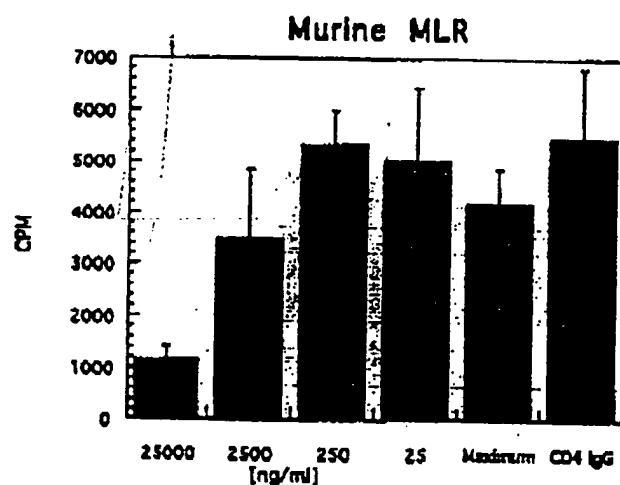


Fig. 11B

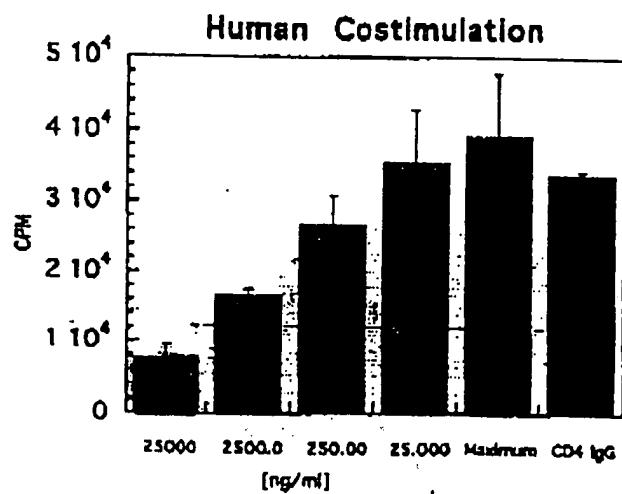


Fig. 11C

FIGURE 12

<u>mAb</u>	<u>Isotype</u>	Antigen Specificity (ELISA)					% Blocking (ELISA)
		DcR3	DR4	DR5	DcR1	OPG	
4B7.1.1	IgG1	+++	-	-	-	-	+
4C4.1.4	IgG2a	+++	-	-	-	-	-
5C4.14.7	IgG2b	+++	-	-	-	-	++
8D3.1.5	IgG1	+++	-	-	-	-	+/-
11C5.2.8	IgG1	+++	-	-	-	-	++

Antigen specificity was determined using 10 microgram/ml mAb.

% blocking activity was determined by ELISA at 100 fold excess of mAb to Fas ligand.

Fig. 13

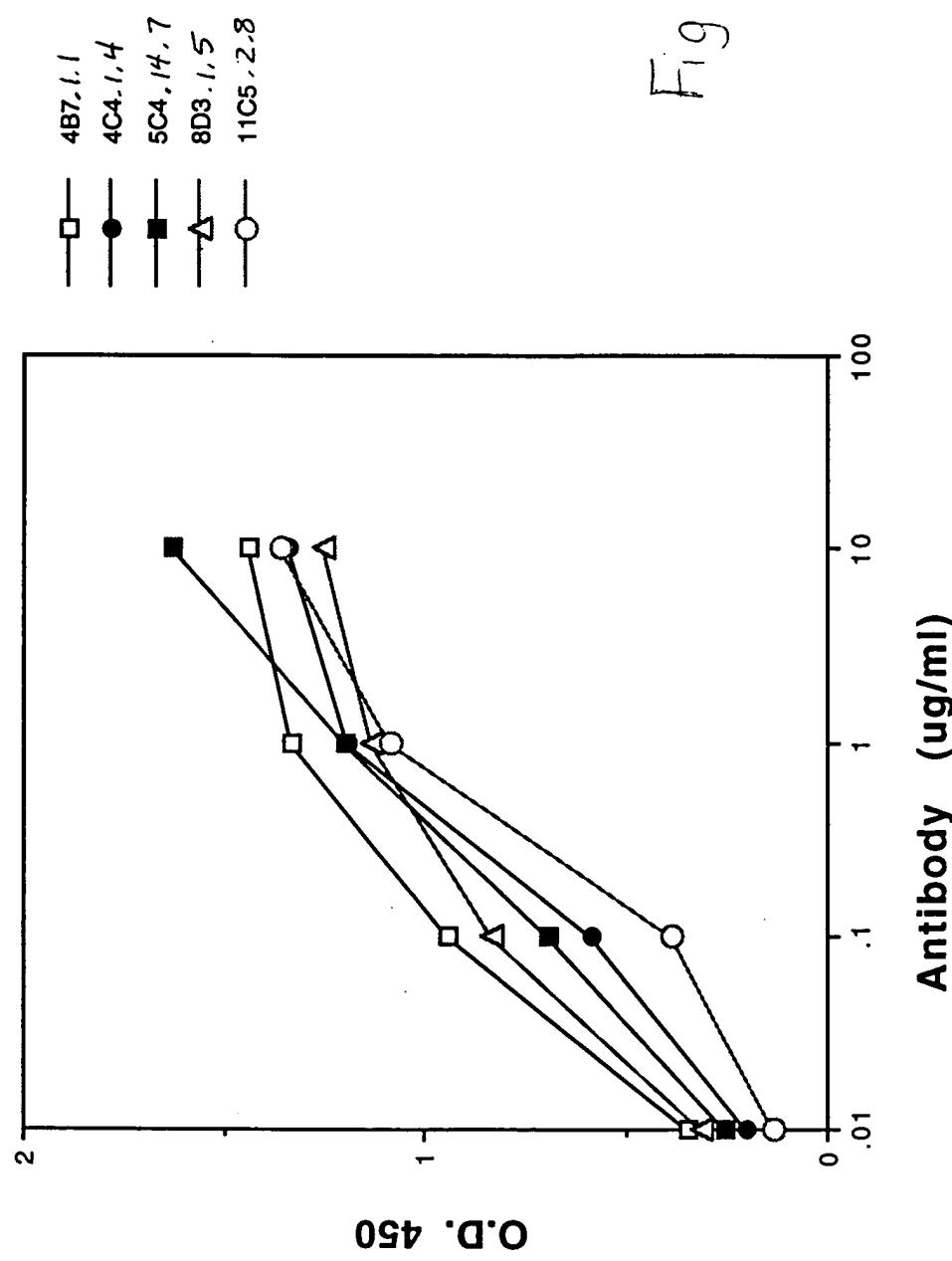


Fig. 14

